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OM protein - protein search, using sw model

Run on: May 19, 2003, 16:36:02 ; Search time 15.7956 Seconds  
(without alignments)  
982.052 Million cell updates/sec

Title: US-09-625-573-2  
Perfect score: 1970  
Sequence: 1 MLSTSRFRFRINTNESGEV.....GKGKSGRAPEASLQDKEGA 374

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1970	100.0	374	1	CKR2_HUMAN
2	1614.5	82.0	360	1	CKR2_MACMU
3	1346.5	68.4	373	1	CKR2_RAT
4	1332.5	67.6	373	1	CKR2_MOUSE
5	1244	63.1	354	1	CKP5_MOUSE
6	1236	62.7	352	1	CKP5_CERTO
7	1236	62.7	352	1	CKR5_HYLL
8	1230	62.4	352	1	CKR5_MACMU
9	1230	62.4	352	1	CKR5_PANTR
10	1230	62.4	352	1	CKR5_PONPY
11	1230	62.4	354	1	CKR5_RAT
12	1228	62.3	352	1	CKR5_GORGO
13	1228	62.3	352	1	CKR5_PAPHA
14	1224	62.1	352	1	CKR5_HUMAN
15	1224	62.1	352	1	CKR5_PYGNE
16	1223	62.1	352	1	CKR5_PYGBI
17	1223	62.1	352	1	CKR5_TRAFR
18	1223	62.1	352	1	CKR5_TAPH
19	1211	61.5	352	1	CKR5_CERAE
20	967.5	49.1	355	1	CKR1_HUMAN
21	951.5	48.3	359	1	CKR3_MOUSE
22	945	48.0	359	1	CKR3_RAT
23	931.5	47.3	358	1	CKR3_CAVPO
24	911.5	46.3	355	1	CKR1_MACMU
25	899.5	45.7	355	1	CKR1_MOUSE
26	886.5	45.0	355	1	CKR3_HUMAN
27	876	44.5	355	1	CKR3_MACMU
28	867	44.0	355	1	CKR3_CERAE
29	833	42.3	360	1	CKR4_MOUSE
30	831.5	42.2	360	1	CKR4_HUMAN
31	731	37.1	356	1	CKRV_MOUSE
32	723	36.7	355	1	CKR8_HUMAN
33	716.5	36.4	356	1	CKR8_MACMU

34 708.5 36.0 353 1 CKR8\_MOUSE  
35 704.5 35.8 354 1 C3X1\_RAT  
36 698 35.4 355 1 C3X1\_HUMAN  
37 692 35.1 354 1 C3X1\_MOUSE  
38 588 29.8 384 1 CKD6\_HUMAN  
39 584 29.6 378 1 CKR7\_HUMAN  
40 580 29.4 378 1 CKD6\_MOUSE  
41 575.5 29.2 378 1 CKR7\_MOUSE  
42 575 29.2 382 1 CKD6\_RAT  
43 569 28.9 357 1 CKR9\_HUMAN  
44 564 28.6 367 1 CKR6\_MOUSE  
45 563 28.6 369 1 CKR9\_MOUSE

## ALIGNMENTS

RESULT 1  
ID CKR2\_HUMAN STANDARD; PRT; 374 AA.  
AC P41597;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE C-C chemokine receptor type 2 (C-CR2) (CCR-2) (CCR2)  
DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).  
GN CCR2 OR CMKBR2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94195821; PubMed=8146186;  
RA Charo I.F., Myers S.J., Herman A., Franci C., Connolly A.J.,  
RA Coughlin S.R.;  
RA "Molecular cloning and functional expression of two monocyte  
RT chemoattractant protein 1 receptors reveals alternative splicing of  
RT the carboxyl-terminal tails";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:2752-2756(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9434942; PubMed=8048929;  
RA Yamagami S., Tokuda Y., Ishii K., Tamaka H., Endo N.;  
RT "CDNA cloning and functional expression of a human monocyte  
RT chemoattractant protein 1 receptor";  
RL Biochem. Biophys. Res. Commun. 202:1156-1162(1994).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97150864; PubMed=8995400;  
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;  
RT "Organization and differential expression of the human monocyte  
RT chemoattractant protein 1 receptor gene. Evidence for the role of the  
RT carboxyl-terminal tail in receptor trafficking";  
RL J. Biol. Chem. 272:1038-1045(1997).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97150864; PubMed=8995400;  
RA Wong L.-M., Myers S.J., Tsou C.-L., Gosling J., Arai H., Charo I.F.;  
RT "Organization and differential expression of the human monocyte  
RT chemoattractant protein 1 receptor gene. Evidence for the role of the  
RT carboxyl-terminal tail in receptor trafficking";  
RL J. Biol. Chem. 272:1038-1045(1997).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20501133; PubMed=11046064;  
RA Preobrazhensky A.A., Dragan S., Kawano T., Gavrilin M.A., Gulina I.V.,  
RA Chakravarty L., Kolattukudy P.E.;  
RT "Monocyte chemotactic protein-1 receptor CCR2B is a glycoprotein that  
RT has tyrosine sulfation in a conserved extracellular N-terminal  
RT region";  
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

J. Immunol. 165:5295-5303(2000).

CC -1- FUNCTION: Receptor for the MCP-1, MCP-3 and MCP-4 chemokines.  
 CC Transduces a signal by increasing the intracellular calcium ions  
 CC level. Alternative coreceptor with CD4 for HIV-1 infection.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- PTM: N-GLYCOSYLATED.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; U03882; AAA19119.1; -  
 DR EMBL; U03905; AAA19120.1; -  
 DR EMBL; D29984; BAA06253.1; -  
 DR EMBL; U80924; AAC51637.1; -  
 DR EMBL; U80924; AAC51636.1; -  
 DR EMBL; U95626; AAB57791.1; -  
 DR EMBL; U95626; AAB57792.1; -  
 DR Genew; HGNC:1603; CCR2.  
 DR MIM; 601267; -  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Alternative splicing.  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 43 70 1 (POTENTIAL).  
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 100 2 (POTENTIAL).  
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 115 136 3 (POTENTIAL).  
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 154 178 4 (POTENTIAL).  
 FT DOMAIN 179 206 5 (POTENTIAL).  
 FT TRANSMEM 207 226 6 (POTENTIAL).  
 FT DOMAIN 227 243 7 (POTENTIAL).  
 FT TRANSMEM 244 268 8 (POTENTIAL).  
 FT DOMAIN 269 285 9 (POTENTIAL).  
 FT TRANSMEM 286 309 10 (POTENTIAL).  
 FT DOMAIN 310 374 11 (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT MOD\_RES 26 26 SULFATION.  
 FT DISULFD 113 190 BY SIMILARITY.  
 FT VARSPIC 314 374 SLFIALGCRAPLQKPVCGGVRPKNVKVTQGLDGR  
 FT GKGSGIGRAPEASLDQKEGA -> RYLVSFFRRKHITKRECK  
 FT QCPVYRETVDCVTSITNPSTGGEQVSAGL (IN  
 FT ISOFORM B).  
 SQ SEQUENCE 374 AA; 41914 MW; F865E0D39E74CF0F CRC64;  
 Query Match 100.0%; Score 1970; DB 1; Length 374;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-115;  
 Matches 374; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFGVGN 60  
 Db 1 MLSTSRFRIRNTNSESGETTFFDYDYGAPCHKFDVKQIGAOQLLPPLYSLVFIFGVGN 60  
 Qy 61 MLVVLINCKKLCTDIYLLNLAISDLFLITPLWAHSAANWVFGNAMCKLETGLY 120  
 Db 61 MLVVLINCKKLCTDIYLLNLAISDLFLITPLWAHSAANWVFGNAMCKLETGLY 120  
 Qy 121 HIGVGGFFFIILLTIDRYLATVHAVFALKARTVFGVVTSVITWLVAVFASVPGIIFTK 180  
 Db 121 HIGVGGFFFIILLTIDRYLATVHAVFALKARTVFGVVTSVITWLVAVFASVPGIIFTK 180

QY 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLPLLMVICYSGLTKTLRCRNEKKRHR 240  
 Db 181 CQKEDSVYVCGPFPFGWNNFHTIMRNILGLVLPLLMVICYSGLTKTLRCRNEKKRHR 240  
 QY 241 AVRVIETIMVYELFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLGTHCCI 300  
 Db 241 AVRVIETIMVYELFWTPYINIVILLNTFQEFFGLSNCESTSQLDQATQVTTGLGTHCCI 300  
 QY 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGVRPKNVKVTQGLDGRGKSKI 360  
 Db 301 NPIIYAFVGEKFRSLFHIALGCRAPLQKPVCGGVRPKNVKVTQGLDGRGKSKI 360  
 QY 361 GRAPEASLDQKEGA 374  
 Db 361 GRAPEASLDQKEGA 374

RESULT 2  
 CCR2\_MACMU STANDARD; PRT; 360 AA.  
 AC O18793;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-C CCR-2) (CC-CCR-2) (CCR-2) (CCR2)  
 DE (Monocyte chemoattractant protein 1 receptor) (MCP-1-R) (CCR2).  
 GN CCR2 OR CCR2.  
 OS Macaca mulatta (Rhesus macaque).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 CC Cercopithecoidea; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21354176; PubMed=11461684;  
 RA Margulies B.J., Hauer D.A., Clements J.E.;  
 RT "Identification and comparison of eleven rhesus macaque chemokine  
 RT receptors.";  
 RL AIDS Res. Hum. Retroviruses 17:981-986(2001).  
 CC -1- FUNCTION: RECEPTOR FOR THE MCP-1, MCP-3 AND MCP-4 CHEMOKINES.  
 CC TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS  
 CC LEVEL.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; AF013958; AAD11572.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEPTOR\_F1\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEPTOR\_F1\_2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation;  
 KW Alternative splicing.  
 FT DOMAIN 1 42 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 43 70 1 (POTENTIAL).  
 FT DOMAIN 71 80 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 81 100 2 (POTENTIAL).  
 FT DOMAIN 101 114 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 115 136 3 (POTENTIAL).  
 FT DOMAIN 137 153 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 154 178 4 (POTENTIAL).  
 FT DOMAIN 179 206 5 (POTENTIAL).

FT TRANSMEM 207 226 5 (POTENTIAL).  
 FT DOMAIN 227 243 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 244 268 6 (POTENTIAL).  
 FT DOMAIN 269 285 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 286 309 7 (POTENTIAL).  
 FT DOMAIN 310 360 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 14 14 N-LINKED (GLCNAC... (POTENTIAL).  
 FT MOD\_RES 26 26 SULFATION (BY SIMILARITY).  
 FT DISULFID 113 190 BY SIMILARITY.  
 SQ SEQUENCE 360 AA; 41139 MW; 4B2552BCE913FE9F CRC64;

Query Match 82.0%; Score 1614.5; DB 1; Length 360;  
 Best Local Similarity 96.6%; Pred. No. 3.1e-93;  
 Matches 308; Conservative 4; Mismatches 4; Indels 3; Gaps 1;

QY 1 MLTSRSRFRINTNESGEVTFDDYDYGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60  
 DB 1 MLTSRSRFRINTNGSGEVTFFDDYDYGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60

QY 61 MLVVLILINCKKLCITDIYLLNLAISSDLLFLITPLWAHSAANEWVFGNACKLFTGLY 120  
 DB 61 MLVVLILINCKKLSLDIYLLNLAISSDLLFLITPLWAHSAANEWVFGNACKLFTGLY 120

QY 121 HIGYFGGIFILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 DB 121 HIGYFGGIFILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180

QY 181 COKEDSVYVCGPYFPRGNWNNFHTMRNLGLVLLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 181 CQEDSVYVCGPYFPRGNWNNFHTMRNLGLVLLIMVICYSGILKTLRCRNEKKRHR 240

QY 241 AVRVTIMIVYFLFWTPYNNVILLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300  
 DB 241 AVRVTIMIVYFLFWTPYNNVILLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKFR---SLF 316  
 DB 301 NPIIYAFVGEKFRRLYSMF 319

RESULT 3  
 CKR2-RAT STANDARD; PRT; 373 AA.  
 ID CKR2-RAT  
 AC O55193;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-CR-2) (CC-CR-2) (CCR2).  
 EN CCR2 OR CMKBR2.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=98318173; PubMed=9655467;  
 RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
 RA defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
 RT "Chemokine receptor expression in cultured glia and rat experimental  
 RT allergic encephalomyelitis";  
 RL J. Neuroimmunol. 86:1-12(1998).  
 CC -!- FUNCTION: RECEPTOR FOR THE MCP-1 (JE), MCP-3 (FIC) AND MCP-5  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LUNG, SPLEEN, KIDNEY, THYMUS AND  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- CALCIUM IONS LEVEL (BY SIMILARITY).  
 CC -!- CHEMOKINES. TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR  
 CC -!- INDUCTION: IN ANIMALS IN WHICH EXPERIMENTAL ALLERGIC  
 CC -!- ENCEPHALOMYELITIS (EAE) HAS BEEN INDUCED.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 CC EMBL: U77349; AAC03242.1;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm1; 1.  
 DR PRINTS: PR00237; GPCRHHODPSN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS0262; G-PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Transmembrane.  
 FT DOMAIN 1 60  
 FT TRANSMEM 61 81  
 FT DOMAIN 82 91  
 FT TRANSMEM 92 112  
 FT DOMAIN 113 128  
 FT TRANSMEM 129 149  
 FT DOMAIN 150 170  
 FT TRANSMEM 171 191  
 FT DOMAIN 192 220  
 FT TRANSMEM 221 241  
 FT DOMAIN 242 256  
 FT TRANSMEM 257 277  
 FT DOMAIN 278 301  
 FT TRANSMEM 302 322  
 FT DOMAIN 323 373  
 FT DISULFID 126 203  
 SQ SEQUENCE 373 AA; 42763 MW; 2E7BB012F5D6FD09 CRC64;

Query Match 68.4%; Score 1346.5; DB 1; Length 373;  
 Best Local Similarity 76.9%; Pred. No. 1.1e-76;  
 Matches 257; Conservative 25; Mismatches 45; Indels 7; Gaps 3;

QY 1 MLTSRSRFRINTNESGEVTFDDYDYGAPCHFDVKGQGAQLPPLSLVIFGFVGN 60  
 DB 14 ILTSHSLFPRSTQELDEGATPDYDDEGCHKTSVKQIGAWILPPLSLVIFGFVGN 73

QY 61 MLVVLILINCKKLCITDIYLLNLAISSDLLFLITPLWAHSAANEWVFGNACKLFTGLY 120  
 DB 74 MLVVLILINCKKLSMTDIYLLNLAISSDLLFLITPLWAHSAANEWVFGNACKLFTGLY 133

QY 121 HIGYFGGIFILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
 DB 134 HIGYFGGIFILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 193

QY 181 COKEDSVYVCGPYFPRGNWNNFHTMRNLGLVLLIMVICYSGILKTLRCRNEKKRHR 240  
 DB 194 SEQEDDQHTCGPYFPTWKNFQIMRNILSLILPPLVWVICYSGILHTLFRCRNEKKRHR 253

QY 241 AVRVTIMIVYFLFWTPYNNVILLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 300  
 DB 254 AVRVTIMIVYFLFWTPYNNVILLNTFQEFGLSNCESTSQDQATQVTTGLMTHCCI 313

QY 301 NPIIYAFVGEKFR---SLF---HIALG-CRIAPL 327  
 DB 314 NPIIYAFVGEKFRRLYSMF 347

RESULT 4  
 CKR2-MOUSE STANDARD; PRT; 373 AA.  
 ID CKR2-MOUSE  
 AC P51683; O61172;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE C-C chemokine receptor type 2 (C-CR-2) (CC-CR-2) (CCR2)  
 DE (JE/FIC receptor) (MCP-1 receptor).  
 GN Mus musculus (Mouse).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



RA MEDLINE=98001387; PubMed=9343222;  
 RA Kuhlmann S.E., Platt E.J., Kozak S.L., Kabat D.;  
 RT "Polymorphisms in the CCR5 genes of African green monkeys and mice  
 RT implicate specific amino acids in infections by simian and human  
 RT immunodeficiency viruses.";  
 RL J. Virol. 71:8642-8656(1997).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=129;  
 RX MEDLINE=97404635; PubMed=9261347;  
 RX Doranz B.J., Lu Z.H., Rucker J., Zhang T.Y., Sharron M., Cen Y.H.,  
 RA Wang Z.X., Guo H.H., Du J.G., Accavitti M.A., Doms R.W., Peiper S.C.;  
 RT "Two distinct CCR5 domains can mediate coreceptor usage by human  
 RT immunodeficiency virus type 1.";  
 RL J. Virol. 71:6305-6314(1997).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP Guo B., Kuno K., Hatada A., Matsushima K.;  
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: DETECTED IN MONOCYTE/MACROPHAGE CELL LINES,  
 CC BUT NOT IN NONHEMATOPOETIC CELL LINES.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 DR EMBL; U47036; AAC52454.1; -;  
 DR EMBL; X94151; CAA63867.1; -;  
 DR EMBL; U68565; AAB37273.1; -;  
 DR EMBL; U83327; AAC53386.1; -;  
 DR EMBL; AF022990; AAC53389.1; -;  
 DR EMBL; AF019772; AAB71183.1; -;  
 DR EMBL; D83648; BAA12024.1; -;  
 DR MGD; MGI:107182; Cmkbr5.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1  
 DR PRINTS; PRO00237; GPCRHOODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS0262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Polymorphism.  
 FT DOMAIN 1 32  
 FT TRANSMEM 33 60  
 FT DOMAIN 61 70  
 FT TRANSMEM 71 91  
 FT DOMAIN 92 104  
 FT TRANSMEM 105 126  
 FT DOMAIN 127 143  
 FT TRANSMEM 144 168  
 FT DOMAIN 169 200  
 FT TRANSMEM 201 220  
 FT DOMAIN 221 237  
 FT TRANSMEM 238 262  
 FT DOMAIN 263 279  
 FT TRANSMEM 280 303  
 FT DOMAIN 304 334  
 FT DISULFID 103 180  
 FT CARBOHYD 270 270  
 FT VARIANT 11 11  
 FT VARIANT 62 62  
 FT VARIANT 66 66  
 FT VARIANT 97 97  
 FT VARIANT 109 109  
 FT VARIANT 156 156  
 FT VARIANT 160 160

FT VARIANT 185 185 P -> L.  
 FT VARIANT 213 213 I -> V.  
 FT VARIANT 318 318 I -> M.  
 FT VARIANT 337 337 V -> A.  
 FT CONFLICT 3 3 F -> L (IN REF. 2).  
 FT CONFLICT 80 80 L -> F (IN REF. 2).  
 FT CONFLICT 145 145 N -> I (IN REF. 5).  
 FT CONFLICT 190 190 H -> Y (IN REF. 3).  
 FT CONFLICT 208 208 P -> S (IN REF. 1).  
 SQ SEQUENCE 354 AA; 40863 MW; B4A6B942E88F9CF0 CRC64;  
 Query Match 63.1%; Score 1244; DB 1; Length 354;  
 Best Local Similarity 75.3%; Pred. No. 2.2e-70;  
 Matches 232; Conservative 29; Mismatches 41; Indels 6; Gaps 2;  
 QY 17 GEEVTFDFDYDYG--APCHKFDVKQGAQLLPYLSLVFEGVGNMVLVLLINCKKLK 74  
 DB 5 GSVPTVIYDIDYGMSPCKQKINVKQIAAQLLPYLSLVFEGVGNMVLVLLINCKKLK 64  
 QY 75 CLTDIYLLNLAISSDLLFLITPLWHAHSAANEVFGNAMCKLTGLYHIGYFGIFFILL 134  
 DB 65 SVTDIYLLNLAISSDLLFLITPLWHAHSAANEVFGNAMCKLTGLYHIGYFGIFFILL 124  
 QY 135 TIDRYLAIHVAHFALKARTVFGVTSVITWLVAVFASVGLIFTKCKQEDSVVCGPYF 194  
 DB 125 TIDRYLAIHVAHFALKARTVFGVTSVITWLVAVFASVGLIFTKCKQEDSVVCGPYF 184  
 QY 195 PRG----WNFTIMRNILGLVPLIMVTCYSGILKTLRCRNEKKHRAVRVFTIMI 250  
 DB 185 PHTQYHFWKSFQTLKVMVLSLILPLLVMIITCYSGILTLFCRNEKKHRAVRVFTIMI 244  
 QY 251 VYLFWTPXNIVILLNTFQBFGLSNCESTSQLDQATQVETGLTGMTHCCINPIYAFVGE 310  
 DB 245 VYLFWTPXNIVILLNTFQBFGLSNCESTSQLDQATQVETGLTGMTHCCINPIYAFVGE 304  
 QY 311 KFRSLFHI 318  
 DB 305 KFRSLSV 312  
 RESULT 6  
 CKR5\_CERTO STANDARD; PRT; 352 AA.  
 ID AC 062743; 062744; 062745; 062746;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-CR-5) (CC-CKR-5) (CCR-5) (CCR5).  
 GN CCR5 OR CMKBR5.  
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 OC Cercopithecinae; Cercopithecus.  
 OC NCBI\_TaxID=9531;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Isolate 079, 085, 087, and 089;  
 RX MEDLINE=98321155; PubMed=9656999;  
 RA Chen Z., Gettie A., Ho D.D., Marx P.A.;  
 RT "Primary SIVsm isolates use the CCR5 coreceptor from sooty mangabeys  
 RT naturally infected in west Africa: a comparison of coreceptor usage  
 RT of primary SIVsm, HIV-2, and SIVmac.";  
 RL Virology 246:113-124(1998).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

	EMBL; AF051902; AAC39830.1;	-	G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
CC	EMBL; AF051903; AAC39831.1;	-	
DR	EMBL; AF051904; AAC39832.1;	-	
DR	EMBL; AF051905; AAC39833.1;	-	
DR	InterPro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm_1; 1.		
DR	PRINTS: PR00237; GPCRRHODOPSN		
DR	PROSITE: PS00237; G_PROTEIN_RECEP_Fl_1; 1.		
DR	PROSITE; PS0262; G_PROTEIN_RECEP_Fl_1;		
KW	DOMAIN 1 30	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 31 58	1 (POTENTIAL).	
FT	DOMAIN 59 68	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 69 89	2 (POTENTIAL).	
FT	DOMAIN 90 102	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 103 114	3 (POTENTIAL).	
FT	DOMAIN 125 141	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 142 166	4 (POTENTIAL).	
FT	DOMAIN 167 198	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 199 218	5 (POTENTIAL).	
FT	DOMAIN 219 235	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM 236 260	6 (POTENTIAL).	
FT	DOMAIN 261 277	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 278 301	7 (POTENTIAL).	
FT	DOMAIN 302 352	CYTOPLASMIC (POTENTIAL).	
FT	DISULFID 101 178	BY SIMILARITY.	
FT	MOD_RES 3 3	SULFATION (BY SIMILARITY).	
FT	MOD_RES 10 10	SULFATION (BY SIMILARITY).	
FT	MOD_RES 14 14	SULFATION (BY SIMILARITY).	
FT	MOD_RES 15 15	SULFATION (BY SIMILARITY).	
FT	VARIANT 2 2	D -> E (IN ISOLATE 087).	
FT	VARIANT 3 3	Y -> D (IN ISOLATE 079).	
FT	VARIANT 25 25	M -> V (IN ISOLATE 087).	
FT	VARIANT 100 100	M -> K (IN ISOLATE 079).	
FT	VARIANT 107 107	L -> V (IN ISOLATE 089).	
FT	VARIANT 134 134	V -> G (IN ISOLATE 079).	
FT	VARIANT 146 146	T -> L (IN ISOLATES 085 AND 089).	
FT	VARIANT 340 340	T -> I (IN ISOLATE 079).	
SEQ	SEQUENCE 352 AA; 40489 MW; 20A196E2D47E49CA CRC64;		

RESULT 7

CKR5_HYLLE	STANDARD;	PRT;	352 AA.
ID	CKR5_HYLLE		
AC	O97883;		
DT	30-MAY-2000 (Rel. 39, Created)		
DT	30-MAY-2000 (Rel. 39, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCRS-5).		
GN	CCR5 OR CMKRR5.		
OS	Hyalobates leucogenys (White-cheeked gibbon).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.		
NCBI_TaxID=61853;			
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99416438; PubMed=10486970;		
RT	Zhang Y.-W., Ryder O.A., Zhang Y.-P.;		
RT	"Sequence evolution of the CCR5 chemokine receptor gene in primates.";		
RL	Mol. Biol. Evol. 16:1145-1154(1999).		
CC	-1- FUNCTION: RECEPTOR FOR A C-C-TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,		
CC	MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY		
CC	INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE		
CC	IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR		
CC	DIFFERENTIATION.		
CC	SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
CC			
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CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announcement/">http://www.isb-sib.ch/announcement/</a>		
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		

Query Match	62.7%;	Score	1236;	DB 1:	Length	352;
Best Local Similarity	77.3%;	Pred.	No. 6.9e-70;			
Matches	238;	Conservative	26;	Mismatches	33;	Gaps
12;						
Gaps						
3;						
QY	24	FDDY--GAPCHKFDVKIQGAQLLPLYSLSVIFGVGNMLVLILNCKLIKCLTDIYL	81			
Ddb	10	YDIDYTTSEPCOKINVKQAARLLPLYSLSVIFGVGNILVVILINCKRLKSMTDIYL	69			
QY	82	LNLATSDLLFLTLPLWAHSAANWFGNAMCKLTGLYHYCYFCGIGFIILLTIDRYLA	141			
Ddb	70	LNLATSDLLFLTTFVFAHYAAAQMDFGMTCOLLTGTYIFGFSGIFIIILLTIDRYLA	129			
QY	142	IHVAVFALKARTVTGGVTSVITWLVAVFASVPGLIFTKCQKEDSVYCGPFP----	RG 197			
Ddb	130	IHVAVFALKARTVTGGVTSVITWWVAVFASLPGLIFTRSQREGLHYTCSHPFPY	SQYQF 189			
QY	198	KNNFTTIMRNILGLVLPILLINVICYSGILKTLRCRNEKKRHRAVRVFTIMIVFLPWT	257			
Ddb	190	KNFOTLKIVILGLVLPILVMVICYSGILKTLRCRNEKKRHRAVRVFTIMIVFLFWA	249			
QY	258	PYNIVILLNTFOEPGLNCSTESOLDATOVTETLGTHCCINPIIAFYGKEKRSLF-	316			
Ddb	250	PYNIVILLNTQEFPGLNCCSSNELDQAMQVTELTGMTHCCINPIIAFYGKEKFRNYL	309			
QY	317	-----HIA	319			
Ddb	310	VFFOKHIA	317			



QY 258 PYNIVILLNTFQEFGLSNCSTESQLOQATQVETLGTHTCCINPIIYAFVGEKFRSLF- 316  
 DB 250 PYNIVLLNTFQEFGLSNCSTESQLOQATQVETLGTHTCCINPIIYAFVGEKFRSLF- 309  
 QY 317 -----HIA 319  
 DB 310 VFFQKHIA 317

RESULT 9  
 CKR5\_PANTR STANDARD; PRT; 352 AA.  
 AC P56440; 002778;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).  
 OS CKR5 OR CMKBR5.  
 GN Pan troglodytes (Chimpanzee).  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M.,  
 RA Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M.,  
 RA Peiper S.C., Pantlitz M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic  
 RT simian immunodeficiency virus strains";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Zimmerman P.A., Buckler-White A., Alkhatib G.;  
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98022612; PubMed=9359654;  
 RA Zhang L., Carruthers C.D., He T., Huang Y., Cao Y., Wang B.,  
 RA Ho D.D.;  
 RT "HIV type 1 subtypes, coreceptor usage, and CCR5 polymorphism";  
 RL AIDS Res. Hum. Retroviruses 13:1357-1366(1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97426118; PubMed=9282822;  
 RA Zacharova V., Zachar V., Goustin A.S.;  
 RT "Sequence of chemokine receptor gene CCR5 in chimpanzees, a natural  
 RT HIV type 1 host";  
 RL AIDS Res. Hum. Retroviruses 13:1159-1161(1997).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98090115; PubMed=9430250;  
 RA Pretet J.-L., Zerbib A., Girard M., Guillet J.-G., Butor C.;  
 RT "Chimpanzee CXCR4 and CCR5 act as coreceptors for HIV type 1";  
 RL AIDS Res. Hum. Retroviruses 13:1583-1587(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
 CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
 CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
 CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
 CC DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC -----  
 DR EMBL; AF005663; AAB62557.1; -;  
 DR EMBL; U94329; AAB58446.1; -;

DR EMBL; AF011542; AAB65742.1; -;  
 DR EMBL; U97666; AAC51670.1; -;  
 DR EMBL; AF011540; AAB65740.1; -;  
 DR EMBL; U89797; AAC03717.1; -;  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30  
 FT TRANSMEM 31 58  
 FT DOMAIN 59 68  
 FT TRANSMEM 69 89  
 FT DOMAIN 90 102  
 FT TRANSMEM 103 124  
 FT DOMAIN 125 141  
 FT TRANSMEM 142 166  
 FT DOMAIN 167 198  
 FT TRANSMEM 199 218  
 FT DOMAIN 219 235  
 FT TRANSMEM 236 260  
 FT DOMAIN 261 277  
 FT TRANSMEM 278 301  
 FT DOMAIN 302 352  
 FT DISULFID 101 178  
 FT MOD\_RES 3 3  
 FT MOD\_RES 10 10  
 FT MOD\_RES 14 14  
 FT MOD\_RES 15 15  
 FT CARBOHYD 268 268  
 FT CONFLICT 123 123  
 SQ SEQUENCE 352 AA; 40539 MW; 4A33E698B80FE34C CRC64;

Query Match 62.4%; Score 1230; DB 1; Length 352;  
 Best Local Similarity 76.9%; Pred. No. 1.6e-69;  
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;  
 QY 24 FDYD--CAPCHKFDVKQIAGQALLPLYSLVFFGVGNMVLVLLINCKKLCITDIYL 81  
 DB YDIIDYTTSEPCQKINVKQIAARLLPLYSLVFFGVGNMVLVLLINCKKLSMTDIYL 69  
 QY 82 LNLAISDLLFLITPLWHAASAANEVFGNAMCKLFTGLYHIGYFGGIFITLITIDRYLA 141  
 DB LNLAISDLLFFLTVPFWAHYAAQWDFGNTMCQLTGLYFGFGIFITLITIDRYLA 129  
 QY 142 IVHAVFALKARTVTEGVVTSVITWLVAVFASVPGIITFCOKEDSVVCGPYEP---RG 197  
 DB IVHAVFALKARTVTEGVVTSVITWLVAVFASVPGIITFCOKEDSVVCGPYEP---RG 189  
 QY 198 WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVFTIMIVYFLFWT 257  
 DB WNNFHTIMRNILGLVPLIMVICYSGILKTLRCRNEKKRHRRAVRVFTIMIVYFLFWT 249  
 QY 258 PYNIVILLANTQEFGLSNCSTESQLOQATQVETLGTHTCCINPIIYAFVGEKFRSLF- 316  
 DB PYNIVILLANTQEFGLSNCSTESQLOQATQVETLGTHTCCINPIIYAFVGEKFRSLF- 309  
 QY 317 -----HIA 319  
 DB 310 VFFQKHIA 317

RESULT 10  
 CKR5\_PONPY STANDARD; PRT; 352 AA.  
 ID CKR5\_PONPY  
 AC O97881;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE C-C chemokine receptor type 5 (C-C CKR-5) (CC-CKR-5) (CCR-5).  
 GN CKR5 OR CMKBR5.  
 OS Pongo pygmaeus (Orangutan).



OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.  
OX NCBI\_TaxID=9600;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9416438; PubMed=10486970;  
RA Zhang Y.-W., Ryder O.A., Zhang Y.-P.;  
RT "Sequence evolution of the CKR5 chemokine receptor gene in primates.";  
RL Mol. Biol. Evol. 16:1145-1154(1999).  
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE  
CC IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR  
CC DIFFERENTIATION.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC  
CC EMBL; AF075446; AAD19858.1;  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN\_RECEP\_FL2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 31 58 1 (POTENTIAL).  
FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 69 89 2 (POTENTIAL).  
FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 124 3 (POTENTIAL).  
FT DOMAIN 125 141 4 (POTENTIAL).  
FT TRANSMEM 142 166 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 199 218 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 219 235 6 (POTENTIAL).  
FT TRANSMEM 236 260 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 261 277 7 (POTENTIAL).  
FT TRANSMEM 278 301 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 302 352 BY SIMILARITY.  
FT DISULFID 101 178 SULFATION (BY SIMILARITY).  
FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
FT MOD\_RES 352 AA; 40527 MW; F4E2F47135AF658A CRC64;  
SQ SEQUENCE 352 AA; 62.4%; Score 1230; DB 1; Length 352;  
Query Match 62.4%; Score 1230; DB 1; Length 352;  
Best Local Similarity 76.9%; Pred. No. 1.6e-69;  
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;  
QY 24 FDYD--GAPCHFDVKQIAQLLPPLYSLVIFGFGVGNMLVILILNCKLCLTDIYL 81  
DB 10 YDIDYTTSEPCQKINQIAARLLPPLYSLVIFGFGVGNMLVILILNCKRLKSMTDIYL 69  
QY 82 LNLAIISDLFLIPLWAHSAANEWFGNACMLFTGLYHIGYFGGFIILLITIDRYLA 141  
DB 70 LNLAIISDLFLIPLWAHSAANEWFGNACMLFTGLYHIGYFGGFIILLITIDRYLA 129  
QY 142 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYEP----RG 197  
DB 130 IVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTKCKEDSVVCGPYEP----RG 189  
QY 198 WNNFHTMRLNLGLVPLLLIIVICYSIGILKTLRCRKRHRRAVRVIFTIMIVYFLWT 257  
DB 190 WKNFQTLKIVLGLVPLLVVVICYSIGILKTLRCRKRHRRAVRVIFTIMIVYFLWA 249

QY 258 PYNIVILLNTFOEFFGLSNCESTSLDOATQVTEITLGMTHCCINPIIYAFVGEKFRSLP- 316  
DB 250 PYNIVILLNTFOEFFGLSNCESSNRLDQAMQVTEITLGMTHCCINPIIYAFVGEKFRNYLL 309  
QY 317 -----HIA 319  
DB 310 VFFQKHIA 317  
RESULT 11  
ID CKR5\_RAT STANDARD; PRT; 354 AA.  
AC O08556;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE C-C chemokine receptor type 5 (C-CR-5) (CCR-5) (MIP-1  
DE alpha receptor).  
GN CCR5 OR CNKR5.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Wistar; TISSUE=Brain;  
RX MEDLINE=98334064; PubMed=9670989;  
RA Spleiss O., Gourmal N., Boddeke H.W.G.M., Sauter A., Fiebich B.L.,  
RA Berger M., Gebicke-Haerter P.J.;  
RT "Cloning of rat HIV-1-chemokine coreceptor CCR5 from microglia and  
RT upregulation of its mRNA in ischemic and endotoxinemic rat brain.";  
RL J. Neurosci. Res. 53:16-28(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=Sprague-Dawley;  
RX MEDLINE=98318173; PubMed=9655467;  
RA Jiang Y., Salafra M.N., Adhikari S., Xia Y., Feng L., Sonntag M.K.,  
RA Defebvre C.M., Pennell N.A., Streit W.J., Harrison J.K.;  
RT "Chemokine receptor expression in cultured glia and rat experimental  
RT allergic encephalomyelitis";  
RL J. Neuroimmunol. 86:1-12(1998).  
CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA,  
CC MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY  
CC INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; Y12009; AAC2737.1; -  
CC EMBL; U77350; AAC03243.1; -  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODPSN.  
DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN\_RECEP\_FL2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT DOMAIN 1 32 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 33 60 1 (POTENTIAL).  
FT DOMAIN 61 70 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 71 91 2 (POTENTIAL).  
FT DOMAIN 92 104 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 105 126 3 (POTENTIAL).  
FT DOMAIN 127 143 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 144 168 4 (POTENTIAL).  
FT DOMAIN 169 200 EXTRACELLULAR (POTENTIAL).

TRANSMEM 201 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 262 6 (POTENTIAL).  
 FT DOMAIN 263 279 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 280 303 7 (POTENTIAL).  
 FT DOMAIN 304 354 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 103 180 BY SIMILARITY.  
 FT CARBOHYD 270 270 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 354 AA; 41030 MW; 77EDB368AA4C868D CRC64;

Query Match 62.4%; Score 1230; DB 1; Length 354;  
 Best Local Similarity 75.0%; Pred. No. 1.6e-69;  
 Matches 231; Conservative 29; Mismatches 42; Indels 6; Gaps 2;

QY 17 GEEVTFEDYD--GAPCHKEDVQIGQALLPPLYSLVFIQFVGNMVLVLINCKKLK 74  
 Db 5 GSPTIYIDIDYSAPCQVNNVQIAAQLPPLYSLVFIQFVGNMVLVLINCKKLK 64  
 QY 75 CLTDIYLLNLAISDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIEFIILL 134  
 65 SMTDIYFLNLAISDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIEFIILL 124  
 QY 135 TIDRYLAIVAVFALKARTVTFGVVTSVITWLVAFAVSPGIIFTKCKEDSVVYCGPYF 194  
 Db 125 TIDRYLAIVAVFALKARTVTFGVVTSVITWLVAFAVSPGIIFTKCKEDSVVYCGPYF 184  
 QY 195 ----PRGWNPFHTMRNLGLVPLLLIMVICYSGILKTLRCRNEKKRHRAVRVFTIMI 250  
 Db 185 LHQYRFWKHFQILKWLISLPLLVVICYSGILNTLFCRNEKKRHRAVRVFTIMI 244  
 QY 251 VYFLFTPPYINVLNTFQFFGLNSCESTSQLDAQVTTGLMTHCCINPIYAFVGE 310  
 Db 245 VYFLFTPPYINVLNTFQFFGLNSCESTSQLDAQVTTGLMTHCCINPIYAFVGE 304  
 QY 311 KFRSLRPHI 318  
 Db 305 KFRNLSV 312

RESULT 12  
 ID CKR5 GORGO STANDARD; PRT; 352 AA.  
 AC P56439;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN C-C chemokine receptor type 5 (C-C CR-5) (CC-CR-5) (CCR-5) (CCR5).  
 GN Gorilla gorilla gorilla (Lowland gorilla).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.  
 OX NCBI\_TaxID=9595;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97268687; PubMed=9108095;  
 RA Edinger A.L., Amedee A., Miller K., Doranz B.J., Endres M., Sharron M., Samson M., Lu Z.H., Clements J.E., Murphy-Corb M., Peiper S.C., Parmentier M., Broder C.C., Doms R.W.;  
 RT "Differential utilization of CCR5 by macrophage and T cell tropic simian immunodeficiency virus strains".  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:4005-4010(1997).  
 CC -!- FUNCTION: RECEPTOR FOR A C-C TYPE CHEMOKINE. BINDS TO MIP-1-ALPHA, MIP-1-BETA AND RANTES AND SUBSEQUENTLY TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS LEVEL. MAY PLAY A ROLE IN THE CONTROL OF GRANULOCYTIC LINEAGE PROLIFERATION OR DIFFERENTIATION.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 -----  
 CC EMBL; AF005659; AAB62553.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsn.  
 DR Pfam; PF00001; 7tm.1; 1.  
 DR PRINTS; PR00237; GPCRBDOPS  
 DR PROSITE; PS00237; G-PROTEIN\_RECEP\_FT\_1; 1.  
 DR PROSITE; PS00262; G-PROTEIN\_RECEP\_FT\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.  
 FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 31 58 1 (POTENTIAL).  
 FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 69 89 2 (POTENTIAL).  
 FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 103 124 3 (POTENTIAL).  
 FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 142 166 4 (POTENTIAL).  
 FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 199 218 5 (POTENTIAL).  
 FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 236 260 6 (POTENTIAL).  
 FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 278 301 7 (POTENTIAL).  
 FT DOMAIN 302 352 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 101 178 BY SIMILARITY.  
 FT MOD\_RES 3 3 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 10 10 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 14 14 SULFATION (BY SIMILARITY).  
 FT MOD\_RES 15 15 SULFATION (BY SIMILARITY).  
 SQ SEQUENCE 352 AA; 40515 MW; D0E6FCB9FE5EAC84 CRC64;

Query Match 62.3%; Score 1228; DB 1; Length 352;  
 Best Local Similarity 76.9%; Pred. No. 2.1e-69;  
 Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

QY 24 FDYD--GAPCHKEDVQIGQALLPPLYSLVFIQFVGNMVLVLINCKKLKLTDIYL 81  
 Db 10 YDIDYTSQCKQTNVQIAAQLPPLYSLVFIQFVGNMVLVLINCKKLKLTDIYL 69  
 QY 82 LNLASDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIEFIILLTIDRYLA 141  
 Db 70 LNLASDLLFLITLPLWAHSAANEVFNAMCKLFTGLYHIGYGGIEFIILLTIDRYLA 129  
 QY 142 IVHAVFALKARTVTFGVVTSVITWLVAFAVSPGIIFTKCKEDSVVYCGPYF ---RG 197  
 Db 130 IVHAVFALKARTVTFGVVTSVITWLVAFAVSPGIIFTKCKEDSVVYCGPYF ---RG 189  
 QY 198 WNNFHTMRNLGLVPLLLIMVICYSGILKTLRCRNEKKRHRAVRVFTIMIYVFLFW 257  
 Db 190 WNFQTLKTVILGLVPLLVVICYSGILKTLRCRNEKKRHRAVRVFTIMIYVFLFW 249  
 QY 258 PYNIVLLNTFQFFGLNSCESTSQLDAQVTTGLMTHCCINPIIYAFVGEKFRSLF - 316  
 Db 250 PYNIVLLNTFQFFGLNSCESTSQLDAQVTTGLMTHCCINPIIYAFVGEKFRSLF 309  
 QY 317 -----HIA 319  
 Db 310 VFFQKHIA 317

RESULT 13  
 ID CKR5 PAPHA STANDARD; PRT; 352 AA.  
 AC P56441;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN C-C chemokine receptor type 5 (C-C CR-5) (CC-CR-5) (CCR-5) (CCR5).  
 GN Papio hamadryas (Hamadryas baboon), and  
 OS Papio anubis (Olive baboon).

	FT	MOD_RES	14	14	SULFATION (BY SIMILARITY).
	FT	MOD_RES	15	15	SULFATION (BY SIMILARITY).
	FT	CARGOHDYD	268	268	N-LINKED (GLCNAC... ) (POTENTIAL).
	SEQ	SEQUENCE	352 AA; 40489 MW;	SEI504A9BA1FE8B2 CRC64;	
	 Query Match                  62.3%; Score 1228; DB 1; Length 352; Best Local Similarity    76.9%; Pred. No. 2.le-69; Matches 237; Conservative 26; Mismatches 33; Indels 12; Gaps				
QY	24	FDDY--GAPCHKFDVKGTAOLIPLYSLVFIFGVGNMLVLINCKKlLCTDIYL	81	:	:    :
Dd	10	IDYTSTPECCOKINVKYAAARLLPLYSIVLFIFGVGNLVLLINCKRLKSMTDIYL	69	: :	:    :
QY	82:	LNLAIISDLLFLITLPWAHSAANEWFVGNAKLFGTHYGICFYGGIFFILLTIDRYLA	141	:	:    :
Dd	70	LNLAISDLLFLITVPFAHYAAAQWDFGMTCOLLTGLYFIGFFSGIFFILLTIDRYLA	129	:	:    :
QY	142	IYHAVFALKARTVTFGVVTSITWLVAVASPVGIIFTCKOKEDSVWGCPYEP---	RG 197	:	:    :
Dd	130	IYHAVFALKARTVTFGVVTSIIWWAVASPUPIIFTRSQEHLHTCSSHPFSYQQF	189	:	:    :
QY	198	WNPHPTIMRNTLGVLPLIMVICYSIGILKTLLRCRNKKRRRAVRVIETMIVVFLFWT	257	:	:    :
Dd	190	WKNFQTIKVIGELGPLLVLMVICYSIGILTLCRCNKRKHRAVRLIFTMIIVVLEWA	249	:	:    :
QY	258	PYNIVILLNTFOBFGLSNCESSTSOLDQAOTVTTGTGLMGTHCCINCPIIAAFVEKEFRSLF-	316	:	:    :
Dd	250	PYNIVILLNTFOBFGLLNCSNSNRDLDAQOVTETLGMTHCCINCPIIAAFVEKEFRNYLL	309	:	:    :
QY	317	-----HTA 319 			
Dd	310	VFKQHHA 317 			
RESULT 14					
ID	CRK5_HUMAN	STANDARD; PRT; 352 AA.			
AC	P51681; O14692; O14693; O14695; O14696; O14697; O14698; O14699;				
AC	O14700; O14701; O14702; O14703; O14704; O14705; O14706; O14707;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DE	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	C-C chemokine receptor type 5 (C-C CKR-5) (CCR-5) (CCR5)				
DE	(HIV-1 fusion co-receptor) (CHEMR13) (CD195 antigen).				
OS	CRK5 OR CMKBRS.				
ON	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
EN	[1]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=96241590; PubMed=8639485;				
RX	Samson M., Labbe O., Molereau C., Vassart G., Parmentier M.;				
RA	"Molecular cloning and functional expression of a new human				
RT	CC-chemokine receptor gene."				
RL	Biochemistry 35:3362-3367(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96291862; PubMed=8663314;				
RA	Raport C.-J., Gosling J., Schweichart V.L., Gray P.W., Charo I.F.;				
RT	"Molecular cloning and functional characterization of a novel human				
RT	CC chemokine receptor (CCR5) for RANTES, MIP-lbeta, and MIP-lalpha,"				
RL	J. Biol. Chem. 271:17161-17166(1996).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96295970; PubMed=8699119;				
RA	Combiadriere C., Ahuja S.K., Tiffany H.L., Murphy P.M.;				
RT	"Cloning and functional expression of CC CRK5, a human monocyte CC				
RT	chemokine receptor selective for MIP-1(alpha), MIP-1(beta), and				
RT	RANTES;"				
RL	J. Leukoc. Biol. 60:147-152(1996).				
RN	[4]				



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CC CC -----
CC CC EMBL: AF075448; AAD19860.1; -.
DR DR InterPro: IPR000276; GPCR_Rhodpsn.
DR DR Pfam: PF00001; 7tm_1; 1.
DR DR PRINTS: PR00237; GPCRRHODOPSN.
DR DR PROSITE: PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR DR PROSITE: PS00262; G_PROTEIN_RECEP_FL_2; 1.
KW KW G-protein coupled receptor; Transmembrane; Glycoprotein; Sulfation.
FT FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL)...
FT FT TRANSMEM 31 58 1 (POTENTIAL);
FT FT DOMAIN 59 68 CYTOPLASMIC (POTENTIAL);
FT FT TRANSMEM 69 89 2 (POTENTIAL);
FT FT DOMAIN 90 102 EXTRACELLULAR (POTENTIAL);
FT FT TRANSMEM 103 124 3 (POTENTIAL);
FT FT DOMAIN 125 141 CYTOPLASMIC (POTENTIAL);
FT FT TRANSMEM 142 166 4 (POTENTIAL);
FT FT DOMAIN 167 198 EXTRACELLULAR (POTENTIAL);
FT FT TRANSMEM 199 218 5 (POTENTIAL);
FT FT DOMAIN 219 235 CYTOPLASMIC (POTENTIAL);
FT FT TRANSMEM 236 260 6 (POTENTIAL);
FT FT DOMAIN 261 277 EXTRACELLULAR (POTENTIAL);
FT FT TRANSMEM 278 301 7 (POTENTIAL);
FT FT DOMAIN 302 352 BY SIMILARITY;
FT FT DISULFID 101 178 SULFATION (BY SIMILARITY);
FT FT MOD_RES 3 3 SULFATION (BY SIMILARITY);
FT FT MOD_RES 10 10 SULFATION (BY SIMILARITY);
FT FT MOD_RES 14 14 SULFATION (BY SIMILARITY);
FT FT MOD_RES 15 15 SULFATION (BY SIMILARITY);
SQ SEQUENCE 352 AA; 40532 MW; FE4F9D98D3B3E861 CRC64;

Query Match      62.1%; Score 1224; DB 1; Length 352;
Best Local Similarity 76.9%; Pred. No. 3.8e-69;
Matches 237; Conservative 25; Mismatches 34; Indels 12; Gaps 3;

Qy 24 PDYDY--GAPCHKFDVKQTGAQLLPPLYSLVFIQFGVGNMLVLILNCKKLCLTDIYL 81
Db   : || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    10 YDIIDYTSEPCOKVNKQIAEARLLPPLYSLVFIQFGVGNILVVILINCKRUKSMTDIYL 69

Qy 82 LNLAISDLLFLTLPLWAHSANENWFGNAMCKLTGLYGHYGFQGIIFILLTTIDRYLA 141
Db   : || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    70 LNLAISDLFFLTVPFWAHYAQAOWDFGNTMCOLLTGLYFGFFSGIFILLTTIDRYLA 129

Qy 142 IVHAVFALKARTVTGVTSVITWLVAVFASVPGIIIFTKCQEDSVVVGPPYFP----RG 197
Db   : || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    130 IVHAVFALKARTVTGVTSVITWWAVFASLPGIIIFRSOREGLHYTCSSHEPYSQYQF 189

Qy 198 WNNFHITIMRNILGLVPLLIMVCYSGILKTLRLCRNEKKRHRAVRVITFMIVFLFWT 257
Db   : || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    190 WKNFQTKLVIGLVPLLIMVCYSGILKTLRLCRNEKKRHRAVRLEITFMIVFLFWA 249

Qy 258 PYNIVILLNTFOEFFGLSNCESTSOLDQAOTVETLGMTHCCINPIIYAFVGEKPRSLE- 316
Db   : || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    250 PYNIVILLNTFOEFFGLNCSNRUDQAOMQVETLGMTHCCINPIIYAFVGEKFRNYLL 309

Qy 317 ----HIA 319
Db   : |||
    310 VFQKHIA 317

Search completed: May 19, 2003, 16:46:13
Job time : 16.7956 secs

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